

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2007, 15:20:33 ; Search time 0.001 Seconds  
(without alignments)  
25.696 Million cell updates/sec

Title: US-10-814-760A-4  
Perfect score: 22  
Sequence: 1 gcgccgctaaaatgcgactga 22  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 584 residues  
Total number of hits satisfying chosen parameters: 2  
Minimum DB seq length: 0  
Maximum DB seq length: 20000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : seqidl.seq: \*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
c	1	20	90.9	584 1 US-10-814-760A-1
	2	11	50.0	584 1 US-10-814-760A-1

ALIGNMENTS

RESULT 1  
US-10-814-760A-1  
; Sequence 1, Application US/10814760A  
; GENERAL INFORMATION:  
; APPLICANT: Buchanan, Fiona C.  
; APPLICANT: Thue, Tracy D.  
; APPLICANT: Winkelman-Sim, Dianne  
; TITLE OF INVENTION: CRH AND POMC EFFECTS ON ANIMAL GROWTH  
; FILE REFERENCE: 0100024.0523741  
; CURRENT APPLICATION NUMBER: US/10/814,760A  
; CURRENT FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (22)...(22)  
; OTHER INFORMATION: SNP present (CRH4")  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (145)...(145)  
; OTHER INFORMATION: SNP present (CRH 45")  
; FEATURE:

; NAME/KEY: misc feature  
; LOCATION: (240)...(240)  
; OTHER INFORMATION: SNP present ("CRH77")  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AF340152  
; DATABASE ENTRY DATE: 2004-02-12  
US-10-814-760A-1

Query Match 90.9%; Score 20; DB 1; Length 584;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CGCCGCTAAAATGCGACTG 21  
Db 1 CGCCGCTAAAATGCGACTG 20

RESULT 2  
US-10-814-760A-1/c  
; Sequence 1, Application US/10814760A  
; GENERAL INFORMATION:  
; APPLICANT: Buchanan, Fiona C.  
; APPLICANT: Thue, Tracy D.  
; APPLICANT: Winkelman-Sim, Dianne  
; TITLE OF INVENTION: CRH AND POMC EFFECTS ON ANIMAL GROWTH  
; FILE REFERENCE: 0100024.0523741  
; CURRENT APPLICATION NUMBER: US/10/814,760A  
; CURRENT FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (22)...(22)  
; OTHER INFORMATION: SNP present (CRH4")  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (145)...(145)  
; OTHER INFORMATION: SNP present ("CRH 45")  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (240)...(240)  
; OTHER INFORMATION: SNP present ("CRH77")  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AF340152  
; DATABASE ENTRY DATE: 2004-02-12  
US-10-814-760A-1

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Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 3 GCCCGCTAAAATGCGACTG 21  
Db 317 GTCCGAGAAAGCGACTG 299

Search completed: January 24, 2007, 15:20:34  
Job time : 1 secs



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OM nucleic - nucleic search, using sw model

Run on: January 24, 2007, 15:20:33 ; Search time 0.001 Seconds  
(without alignments)  
23.360 Million cell updates/sec

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Query Match      100.0%; Score 20; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ? search tips Journal/book title  Volume  Issue  Page  Clear  Go 


results 1 - 24



## 24 Articles Found

pub-date &gt; 1994 and pub-date &lt; 2004 and bovine CRH gene polymorphism detection

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-  1. 



**Leptin signaling in the hypothalamus: emphasis on energy homeostasis and leptin resistance • ARTICLE**

*Frontiers in Neuroendocrinology, Volume 24, Issue 4, December 2003, Pages 225-253*

Abhiram Sahu

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-  2. 



**DAX1 and its network partners: exploring complexity in development • SHORT SURVEY**

*Molecular Genetics and Metabolism, Volume 80, Issues 1-2, September-October 2003, Pages 81-120*

Robert Clipsham and Edward R. B. McCabe

[SummaryPlus](#) | [Full Text + Links](#) | [PDF \(810 K\)](#)

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-  3. 



**Neuroendocrine facets of human puberty • ARTICLE**

*Neurobiology of Aging, Volume 24, Supplement 1, May-June 2003, Pages S93-S119*

Johannes D. Veldhuis

[SummaryPlus](#) | [Full Text + Links](#) | [PDF \(492 K\)](#)

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-  4. 



**Molecular defects in the pathogenesis of pituitary tumours • ARTICLE**

*Frontiers in Neuroendocrinology, Volume 24, Issue 2, April 2003, Pages 94-127*

Andy Levy and Stafford Lightman

[SummaryPlus](#) | [Full Text + Links](#) | [PDF \(605 K\)](#)



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-  5. 

**Poster sessions—Basic science • CALENDAR**

*Gastroenterology, Volume 124, Issue 4, Supplement 1, April 2003, Pages P88-P257*

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-  6. 



**Neuroendocrine pharmacology of stress • ARTICLE**

*European Journal of Pharmacology, Volume 463, Issues 1-3, 28 February 2003, Pages 235-272*

Gonzalo A. Carrasco and Louis D. Van de Kar

[SummaryPlus](#) | [Full Text + Links](#) | [PDF \(620 K\)](#)



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-  7. 

**Subject Index • MISCELLANEOUS**

*International Review of Neurobiology, Volume 58, 2003, Pages 1-294*

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 results 1 - 35

## 35 Articles Found





pub-date &gt; 1994 and pub-date &lt; 2004 and CRH gene polymorphism AND bovine



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 **Search Within Results**

 = Full-text available  = Non-subscribed  What does this mean?

**Article List**



Full Abstracts

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Sort By:   **Go**

-  1. 



**Leptin signaling in the hypothalamus: emphasis on energy homeostasis and leptin resistance • ARTICLE**  
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 Abhiram Sahu  
[SummaryPlus](#) | [Full Text + Links](#) | [PDF \(757 K\)](#)

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 Robert Clipsham and Edward R. B. McCabe  
[SummaryPlus](#) | [Full Text + Links](#) | [PDF \(810 K\)](#)

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-  3. 



**Endogenous opiates and behavior: 2002 • REVIEW ARTICLE**  
*Peptides, Volume 24, Issue 8, August 2003, Pages 1241-1302*  
 Richard J. Bodnar and Maria M. Hadjimarkou  
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-  4. 



**Neuroendocrine facets of human puberty • ARTICLE**  
*Neurobiology of Aging, Volume 24, Supplement 1, May-June 2003, Pages S93-S119*  
 Johannes D. Veldhuis  
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**Poster sessions—Basic science • CALENDAR**  
*Gastroenterology, Volume 124, Issue 4, Supplement 1, April 2003, Pages P88-P257*

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-  7. 

**Neuroendocrine pharmacology of stress • ARTICLE**  
*European Journal of Pharmacology, Volume 463, Issues 1-3, 28 February 2003, Pages 235-272*

# SCORE - View Sequence Detail(s) for Application 10814760

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Enter SEQ ID Here is the list of the requested sequences:

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<110> APPLICANT: Buchanan, Fiona C.  
Thue, Tracy D.  
Winkelman-Sim, Dianne  
<120> TITLE OF INVENTION: CRH AND POMC EFFECTS ON ANIMAL GROWTH  
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catcacagca ccgccagccc ctgagtttct tccagccgcc gccgcagccc caggaaacccc 180  
aggctctgcc caccctactc cgtgttgggg aggaataact cctccgcctg ggtaacctcg 240  
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gccaggaggc gccggccgcc aggaagaggc gatcccagga acctcccatc tccctggatc 480  
tcaccttcca cctcctccga gaagtcttgg aaatgaccaa ggccgatcag ttagcacagc 540  
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<212> TYPE: DNA  
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# SCORE - View Sequence Detail(s) for Application 10814760

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-1 gcgcccgccta aaatgcgact ga

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3' qacactacgg acggcccgctg 5'

20 <BR><BR>

Mismatch to SEQ ID #1 to make Dde I site  
next nucleotide SNP C → G at 22 position.



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Display  Show   Hide: ☐ Sequence ☐ Lesser features

Range: from  to  ☐ Reverse complemented strand Features:

☐ 1: [AF340152](#). Reports *Bos taurus* cortic...[gi:15077524]

[Links](#)

[Features](#) [Sequence](#)

LOCUS AF340152 584 bp DNA linear MAM 18-MAR-2005  
 DEFINITION *Bos taurus* corticotrophin-releasing hormone precursor, gene, exon 2 and complete cds.  
 ACCESSION AF340152  
 VERSION AF340152.1 GI:15077524  
 KEYWORDS .  
 SOURCE *Bos taurus* (cattle)  
 ORGANISM *Bos taurus*  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 584)  
 AUTHORS Buchanan,F.C., Thue,T.D., Yu,P. and Winkelman-Sim,D.C.  
 TITLE Single nucleotide polymorphisms in the corticotrophin-releasing hormone and pro-opiomelanocortin genes are associated with growth and carcass yield in beef cattle  
 JOURNAL Anim. Genet. 36 (2), 127-131 (2005)  
 PUBMED [15771721](#)  
 REFERENCE 2 (bases 1 to 584)  
 AUTHORS Buchanan,F.C., Thue,T.D. and Schmutz,S.M.  
 TITLE Sequence analysis of bovine corticotrophin-releasing hormone - a candidate gene for post-natal growth  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 584)  
 AUTHORS Buchanan,F.C., Thue,T.D. and Schmutz,S.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-JAN-2001) Animal and Poultry Science, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada  
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ORIGIN

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121 catcacagca cccccagccc ctgartttct tccagccgcc gccgcagccc caggaacccc
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421 gccaggaggc gccggccgcc aggaagaggc gatcccagga acctcccatc tccctggatc
481 tcaccttcca cctcctccga gaagtcttgg aaatgaccaa ggccgatcag ttagcacagc
541 aagctcatar caayaggaaa ctgttggaca ttgctgggaa atga
```

//

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Sep 27 2006 15:22:06



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## RELATED INFORMATION

- FAQs for DdeI
- FAQs for Restriction Endonucleases
- Technical Reference for Restriction Endonucleases

## FAVORITE TOOLS

- Enzyme Finder
- NEBcutter
- NEBuffer Chart
- Double Digest Finder
- Isoschizomers
- DNA Sequences and Maps
- REBASE

## RELATED PRODUCTS

- Reagents Sold Separately
- NEBuffer 3

SPECIAL  
OFFERS

## DdeI



Nomenclature Update

Catalog #	Size	Concentration	Price	Qty	
R0175S	500 units	10,000 units/ml	\$53.00	<input type="text" value="1"/>	<input type="button" value="ADD TO CART"/>
R0175L	2,500 units	10,000 units/ml	\$212.00	<input type="text" value="1"/>	<input type="button" value="ADD TO CART"/>

Prices are in US dollars and valid only for US orders.

Download: MSDS PDF

## Recognition Site:

5'...CTNAG...3'  
3'...GANTC...5'

isoschizomers | compatible ends | single letter code

## Source:

A *E. coli* strain that carries the DdeI gene from *Desulfovibrio desulfuricans* (NCIB 83120).

## Reagents Supplied:

NEBuffer 3

## Enzyme Properties

## Activity in NEBuffers:

NEBuffer 1: 75%  
NEBuffer 2: 100%  
NEBuffer 3: 100%  
NEBuffer 4: 75%

When using a buffer other than the optimal (supplied) NEBuffer, it may be necessary to add more enzyme to achieve complete digestion.

## Methylation Sensitivity:

*dam* methylation: Not sensitive  
*dcm* methylation: Not sensitive  
CpG methylation: Not sensitive

## Heat Inactivation:

65°C for 20 minutes

## Survival in a Reaction:

Minimum units to digest 1 µg of substrate DNA in 16 hours: 0.13 unit(s)

## Reaction &amp; Storage Conditions

## Reaction Conditions:

1X NEBuffer 3  
Incubate at 37°C.

## 1X NEBuffer 3:

50 mM Tris-HCl  
100 mM NaCl

# SCORE Search Results Details for Application 10814760 and Search Result 20070116\_103648\_us-10-814- 760a-4.olig.rnpbm.

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This page gives you Search Results detail for the Application 10814760 and Search Result 20070116\_103648\_us-10-814-760a-4.olig.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: January 17, 2007, 14:00:48 ; Search time 786.762 Seconds  
(without alignments)  
343.596 Million cell updates/sec

Title: US-10-814-760A-4  
Perfect score: 22  
Sequence: 1 gcgccccgctaaaatgcgactga 22

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size : 1

Total number of hits satisfying chosen parameters: 37781012

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
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2	20	90.9	584	10	US-10-814-760A-1	Sequence 1, Appli
c 3	15	68.2	594	8	US-10-437-963-24259	Sequence 24259, A
c 4	15	68.2	745	8	US-10-437-963-53950	Sequence 53950, A
c 5	15	68.2	1076	8	US-10-437-963-63645	Sequence 63645, A
6	15	68.2	1149	8	US-10-437-963-89598	Sequence 89598, A
c 7	15	68.2	1612	8	US-10-437-963-81446	Sequence 81446, A
c 8	15	68.2	2000	8	US-10-260-238-1660	Sequence 1660, Ap
c 9	15	68.2	2000	8	US-10-260-238-1756	Sequence 1756, Ap
c 10	15	68.2	2269	8	US-10-437-963-53963	Sequence 53963, A
c 11	14	63.6	137	9	US-10-425-115-144750	Sequence 144750,
c 12	14	63.6	259	9	US-10-425-115-152654	Sequence 152654,
c 13	14	63.6	285	8	US-10-424-599-16415	Sequence 16415, A
14	14	63.6	420	3	US-09-814-353-1151	Sequence 1151, Ap
15	14	63.6	420	3	US-09-814-353-7517	Sequence 7517, Ap
c 16	14	63.6	446	9	US-10-425-115-69598	Sequence 69598, A
c 17	14	63.6	514	8	US-10-437-963-56308	Sequence 56308, A
18	14	63.6	523	3	US-09-814-353-13902	Sequence 13902, A
19	14	63.6	574	4	US-09-925-065A-24596	Sequence 24596, A
20	14	63.6	574	5	US-09-925-065A-24596	Sequence 24596, A
21	14	63.6	574	12	US-10-301-480-125833	Sequence 125833,
22	14	63.6	574	12	US-10-301-480-739242	Sequence 739242,
c 23	14	63.6	779	12	US-10-301-480-558229	Sequence 558229,
c 24	14	63.6	779	12	US-10-301-480-1171638	Sequence 1171638,
c 25	14	63.6	825	8	US-10-437-963-37418	Sequence 37418, A
26	14	63.6	893	10	US-10-450-763-1768	Sequence 1768, Ap
c 27	14	63.6	1024	9	US-10-363-345A-39899	Sequence 39899, A
28	14	63.6	1024	9	US-10-363-345A-39900	Sequence 39900, A
c 29	14	63.6	1024	10	US-10-363-483A-39899	Sequence 39899, A
30	14	63.6	1024	10	US-10-363-483A-39900	Sequence 39900, A
c 31	14	63.6	1041	8	US-10-398-186-13	Sequence 13, Appl
32	14	63.6	1095	6	US-10-198-846-12488	Sequence 12488, A
33	14	63.6	1479	8	US-10-424-599-17902	Sequence 17902, A
c 34	14	63.6	1670	10	US-10-750-185-42347	Sequence 42347, A
c 35	14	63.6	1670	10	US-10-750-623-42347	Sequence 42347, A
c 36	14	63.6	2000	8	US-10-260-238-1866	Sequence 1866, Ap
37	14	63.6	2002	8	US-10-424-599-17891	Sequence 17891, A
38	14	63.6	2578	13	US-11-097-143-12565	Sequence 12565, A
39	14	63.6	4168	13	US-11-097-143-42499	Sequence 42499, A
40	14	63.6	4199	13	US-11-097-143-42523	Sequence 42523, A
c 41	14	63.6	13932	3	US-09-070-927A-363	Sequence 363, App
c 42	14	63.6	28626	8	US-10-672-787-15	Sequence 15, Appl
43	13	59.1	22	11	US-10-310-914A-186688	Sequence 186688,
44	13	59.1	25	11	US-10-933-982-73603	Sequence 73603, A
45	13	59.1	25	13	US-11-036-317-97603	Sequence 97603, A

## ALIGNMENTS

## RESULT 1

US-10-814-760A-4

; Sequence 4, Application US/10814760A

; Publication No. US20050221332A1

; GENERAL INFORMATION:

; APPLICANT: Buchanan, Fiona C.

; APPLICANT: Thue, Tracy D.

; APPLICANT: Winkelman-Sim, Dianne

; TITLE OF INVENTION: CRH AND POMC EFFECTS ON ANIMAL GROWTH

```
; FILE REFERENCE: 0100024.0523741
; CURRENT APPLICATION NUMBER: US/10/814,760A
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Forward primer for DNA amplification of sequences
; OTHER INFORMATION: within SEQ ID NO: 1
US-10-814-760A-4
```

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Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Db      1 GCGCCCGCTAAAATGCGACTGA 22
```

## RESULT 2

US-10-814-760A-1

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; Sequence 1, Application US/10814760A
; Publication No. US20050221332A1
; GENERAL INFORMATION:
; APPLICANT: Buchanan, Fiona C.
; APPLICANT: Thue, Tracy D.
; APPLICANT: Winkelman-Sim, Dianne
; TITLE OF INVENTION: CRH AND POMC EFFECTS ON ANIMAL GROWTH
; FILE REFERENCE: 0100024.0523741
; CURRENT APPLICATION NUMBER: US/10/814,760A
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)...(22)
; OTHER INFORMATION: SNP present (CRH4")
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145)...(145)
; OTHER INFORMATION: SNP present ("CRH 45")
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (240)...(240)
; OTHER INFORMATION: SNP present ("CRH77")
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF340152
; DATABASE ENTRY DATE: 2004-02-12
US-10-814-760A-1
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Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db

|||||  
1 CGCCCGCTAAAATGCGACTG 20

# SCORE Search Results Details for Application 10814760 and Search Result 20070116\_103648\_us-10-814- 760a-5.olig.rnpbm.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10814760 and Search Result 20070116\_103648\_us-10-814-760a-5.olig.rnpbm.

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GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2007, 14:00:48 ; Search time 715.238 Seconds  
(without alignments)  
343.596 Million cell updates/sec

Title: US-10-814-760A-5  
Perfect score: 20  
Sequence: 1 ctgtgatgcctgccgggcac 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size : 1

Total number of hits satisfying chosen parameters: 37781012

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*  
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11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query		DB	ID	Description
	No.	Score Match Length			
	1	20 100.0 20	10	US-10-814-760A-5	Sequence 5, Appli
c	2	20 100.0 584	10	US-10-814-760A-1	Sequence 1, Appli
c	3	18 90.0 195	7	US-10-305-720-947	Sequence 947, App
	4	16 80.0 1081	9	US-10-425-115-26833	Sequence 26833, A
	5	16 80.0 1114	9	US-10-425-115-26838	Sequence 26838, A
c	6	16 80.0 1249	6	US-10-281-024-8	Sequence 8, Appli
	7	15 75.0 494	9	US-10-425-115-31217	Sequence 31217, A
	8	15 75.0 548	8	US-10-021-323-9460	Sequence 9460, Ap
	9	15 75.0 599	4	US-09-925-065A-533756	Sequence 533756,
	10	15 75.0 599	5	US-09-925-065A-533756	Sequence 533756,
	11	15 75.0 629	8	US-10-767-701-26033	Sequence 26033, A
	12	15 75.0 652	8	US-10-767-701-854	Sequence 854, App
	13	15 75.0 714	6	US-10-027-632-23745	Sequence 23745, A
	14	15 75.0 714	7	US-10-027-632-23745	Sequence 23745, A
	15	15 75.0 972	8	US-10-109-310-22	Sequence 22, Appl
	16	15 75.0 985	8	US-10-282-122A-21780	Sequence 21780, A
c	17	15 75.0 1404	8	US-10-417-700A-62	Sequence 62, Appl
	18	15 75.0 1519	8	US-10-425-114-13582	Sequence 13582, A
	19	15 75.0 1612	9	US-10-425-115-108234	Sequence 108234,
	20	15 75.0 7393	6	US-10-037-270-372	Sequence 372, App
	21	15 75.0 7393	7	US-10-117-722-372	Sequence 372, App
	22	15 75.0 7393	10	US-10-122-851-372	Sequence 372, App
c	23	15 75.0 33000	8	US-10-109-310-18	Sequence 18, Appl
	24	15 75.0 159440	12	US-10-960-414-12	Sequence 12, Appl
c	25	14 70.0 19	11	US-10-310-914A-708180	Sequence 708180,
c	26	14 70.0 25	11	US-10-310-914A-708357	Sequence 708357,
	27	14 70.0 25	13	US-11-036-317-136956	Sequence 136956,
	28	14 70.0 118	7	US-10-029-386-19490	Sequence 19490, A
c	29	14 70.0 201	9	US-10-719-993-19236	Sequence 19236, A
c	30	14 70.0 201	9	US-10-741-600-39071	Sequence 39071, A
	31	14 70.0 201	16	US-11-124-367A-20708	Sequence 20708, A
c	32	14 70.0 201	16	US-11-124-367A-34016	Sequence 34016, A
	33	14 70.0 318	9	US-10-425-115-162424	Sequence 162424,
	34	14 70.0 349	9	US-10-425-115-15412	Sequence 15412, A
	35	14 70.0 429	8	US-10-424-599-56364	Sequence 56364, A
c	36	14 70.0 498	6	US-10-051-325-3	Sequence 3, Appli
c	37	14 70.0 498	10	US-10-798-602-3	Sequence 3, Appli
	38	14 70.0 507	4	US-09-925-065A-10912	Sequence 10912, A
	39	14 70.0 507	5	US-09-925-065A-10912	Sequence 10912, A
	40	14 70.0 507	12	US-10-301-480-112149	Sequence 112149,
	41	14 70.0 507	12	US-10-301-480-725558	Sequence 725558,
	42	14 70.0 528	4	US-09-925-065A-58821	Sequence 58821, A
	43	14 70.0 528	5	US-09-925-065A-58821	Sequence 58821, A
	44	14 70.0 528	12	US-10-301-480-160059	Sequence 160059,
	45	14 70.0 528	12	US-10-301-480-773468	Sequence 773468,

## ALIGNMENTS

## RESULT 1

US-10-814-760A-5

; Sequence 5, Application US/10814760A

; Publication No. US20050221332A1

; GENERAL INFORMATION:

; APPLICANT: Buchanan, Fiona C.

; APPLICANT: Thue, Tracy D.

; APPLICANT: Winkelman-Sim, Dianne

; TITLE OF INVENTION: CRH AND POMC EFFECTS ON ANIMAL GROWTH

```
; FILE REFERENCE: 0100024.0523741
; CURRENT APPLICATION NUMBER: US/10/814,760A
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Reverse primer for DNA amplification; sequence is
; OTHER INFORMATION: the reverse complement of the corresponding
; OTHER INFORMATION: sequence in SEQ ID NO: 1
US-10-814-760A-5
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Query Match          100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 CTGTGATGCCTGCCGGGCAC 20
          |||||
Db      1 CTGTGATGCCTGCCGGGCAC 20
```

## RESULT 2

```
US-10-814-760A-1/c
; Sequence 1, Application US/10814760A
; Publication No. US20050221332A1
; GENERAL INFORMATION:
; APPLICANT: Buchanan, Fiona C.
; APPLICANT: Thue, Tracy D.
; APPLICANT: Winkelman-Sim, Dianne
; TITLE OF INVENTION: CRH AND POMC EFFECTS ON ANIMAL GROWTH
; FILE REFERENCE: 0100024.0523741
; CURRENT APPLICATION NUMBER: US/10/814,760A
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)...(22)
; OTHER INFORMATION: SNP present (CRH4")
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145)...(145)
; OTHER INFORMATION: SNP present ("CRH 45")
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (240)...(240)
; OTHER INFORMATION: SNP present ("CRH77")
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF340152
; DATABASE ENTRY DATE: 2004-02-12
US-10-814-760A-1
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Query Match          100.0%; Score 20; DB 10; Length 584;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	CTGTGATGCCTGCCGGGCAC	20
Db	128	CTGTGATGCCTGCCGGGCAC	109

# SCORE Search Results Details for Application 10814760 and Search Result 20070116\_103643\_us-10-814- 760a-5.olig.rst.

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OM nucleic - nucleic search, using sw model

Run on: January 17, 2007, 06:31:46 ; Search time 3680 Seconds  
(without alignments)  
303.909 Million cell updates/sec

Title: US-10-814-760A-5  
Perfect score: 20  
Sequence: 1 ctgtgatgcctgccgggcac 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:\*  
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7: gb\_est2:\*  
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9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query Match Length	DB	ID	Description
	Score	Match				
c 1	20	100.0	669	10	DV826091	DV826091 LB02026.C
c 2	20	100.0	725	10	DV825584	DV825584 LB02023.C
c 3	20	100.0	745	8	CO895988	CO895988 BovGen_24
c 4	20	100.0	762	10	DV822182	DV822182 LB0205.CR
5	18	90.0	698	11	BZ260096	BZ260096 CH230-520
c 6	17	85.0	182	5	CK747358	CK747358 wmi01-6ms
c 7	17	85.0	519	8	CR371468	CR371468 CR371468
8	17	85.0	520	8	CR752169	CR752169 DKFZp469B
c 9	17	85.0	556	4	CA344682	CA344682 675130 NC
c 10	17	85.0	601	4	CA361618	CA361618 635480 NC
c 11	17	85.0	614	4	BX076189	BX076189 BX076189
c 12	17	85.0	660	4	CA344844	CA344844 675322 NC
c 13	17	85.0	689	8	CX138582	CX138582 1277825 N
14	17	85.0	709	11	AZ340142	AZ340142 1M0072P05
c 15	17	85.0	790	10	DT596580	DT596580 wmi03-11m
c 16	17	85.0	1046	14	DU732494	DU732494 APKI1761.
17	16	80.0	501	2	BJ557304	BJ557304 BJ557304
18	16	80.0	537	2	BJ553243	BJ553243 BJ553243
19	16	80.0	539	2	BJ556317	BJ556317 BJ556317
20	16	80.0	542	2	BJ556098	BJ556098 BJ556098
21	16	80.0	545	2	BJ556911	BJ556911 BJ556911
22	16	80.0	580	2	BJ563251	BJ563251 BJ563251
c 23	16	80.0	616	4	CA620605	CA620605 wlln.pk00
24	16	80.0	636	5	CJ742601	CJ742601 CJ742601
25	16	80.0	644	12	CG441261	CG441261 OGVGI69TH
26	16	80.0	674	5	CJ742132	CJ742132 CJ742132
c 27	16	80.0	680	5	CD624435	CD624435 56011177J
c 28	16	80.0	710	2	BM291817	BM291817 EST574359
29	16	80.0	728	5	CJ754476	CJ754476 CJ754476
c 30	16	80.0	767	12	BZ981945	BZ981945 PUFHX46TB
c 31	16	80.0	785	12	CG441267	CG441267 OGVGI69TV
c 32	16	80.0	844	13	CZ355697	CZ355697 ZMMBF0094
33	16	80.0	854	12	CG329718	CG329718 OG1DU35TV
34	16	80.0	880	7	BE035093	BE035093 MM03A09 M
c 35	16	80.0	916	7	BE741437	BE741437 601594419
c 36	16	80.0	1166	7	BE784790	BE784790 601473743
c 37	16	80.0	1414	9	DN715119	DN715119 CNB106-D1
c 38	15	75.0	226	11	AQ008751	AQ008751 RPCI11-22
c 39	15	75.0	259	2	BG955527	BG955527 CM4-CT065
40	15	75.0	292	10	DY238163	DY238163 ZM_BFb025
41	15	75.0	348	10	Z44240	Z44240 HSC1VF071 n
c 42	15	75.0	383	3	BU974891	BU974891 HB29G19r
43	15	75.0	394	3	BQ087267	BQ087267 Cri_10_L0
44	15	75.0	396	4	CB773338	CB773338 AMGNNUC:M
45	15	75.0	397	7	AW265102	AW265102 xp79f07.x

## ALIGNMENTS

RESULT 1  
DV826091/c

LOCUS DV826091 669 bp mRNA linear EST 25-NOV-2005  
DEFINITION LB02026.CR\_G24 GC\_BGC-20 Bos taurus cDNA clone IMAGE:8249522, mRNA sequence.

ACCESSION DV826091

VERSION DV826091.1 GI:82686284

KEYWORDS EST.

SOURCE Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 669)

AUTHORS Moore,S., Alexander,L., Brownstein,M., Guan,L., Lobo,S., Meng,Y.,  
 Tanaguchi,M., Wang,Z., Yu,J., Prange,C., Schreiber,K., Shenmen,C.,  
 Wagner,L., Bala,M., Barbazuk,S., Barber,S., Babakaiff,R.,  
 Beland,J., Chun,E., Del Rio,L., Gibson,S., Hanson,R.,  
 Kirkpatrick,R., Liu,J., Matsuo,C., Mayo,M., Santos,R.R., Stott,J.,  
 Tsai,M., Wong,D., Siddiqui,A., Holt,R., Jones,S.J. and Marra,M.A.

TITLE Bovine Genome Sequencing Program: Full-length cDNA Sequencing

JOURNAL Unpublished (2005)

COMMENT Contact: Robert Kirkpatrick  
 Canada's Michael Smith Genome Sciences Centre  
 BC Cancer Agency  
 Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,  
 Canada, V5Z 4S6  
 Tel: 1-604-707-5900 x5406  
 Fax: 1-604-876-3561  
 Email: robertk@bcgsc.ca  
 Plate: LB02026 row: G column: 24  
 High quality sequence stop: 669.

FEATURES Location/Qualifiers

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 /tissue\_type="Fetal Medulla"  
 /dev\_stage="7 months old fetus"  
 /lab\_host="ElectroMAX DH10B T1 Phage-Resistant Cells"  
 /clone\_lib="GC\_BGC-20"  
 /note="Organ: Fetal Medulla; Vector: pCMV SPORT 6.0;  
 Site\_1: SalI (5' end of cDNA); Site\_2: NotI (3' end of  
 cDNA)"

# ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 669;  
 Best Local Similarity 100.0%; Pred. No. 0.63;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGTGATGCCTGCCGGGCAC 20  
 |||||  
 Db 298 CTGTGATGCCTGCCGGGCAC 279

## RESULT 2

DV825584/c

LOCUS DV825584 725 bp mRNA linear EST 25-NOV-2005

DEFINITION LB02023.CR\_005 GC\_BGC-20 Bos taurus cDNA clone IMAGE:8248543, mRNA  
 sequence.

ACCESSION DV825584

VERSION DV825584.1 GI:82685777

KEYWORDS EST.

SOURCE Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 725)

AUTHORS Moore,S., Alexander,L., Brownstein,M., Guan,L., Lobo,S., Meng,Y.,  
 Tanaguchi,M., Wang,Z., Yu,J., Prange,C., Schreiber,K., Shenmen,C.,  
 Wagner,L., Bala,M., Barbazuk,S., Barber,S., Babakaiff,R.,  
 Beland,J., Chun,E., Del Rio,L., Gibson,S., Hanson,R.,

TITLE Kirkpatrick,R., Liu,J., Matsuo,C., Mayo,M., Santos,R.R., Stott,J.,  
Tsai,M., Wong,D., Siddiqui,A., Holt,R., Jones,S.J. and Marra,M.A.  
JOURNAL Bovine Genome Sequencing Program: Full-length cDNA Sequencing  
COMMENT Unpublished (2005)  
Contact: Robert Kirkpatrick  
Canada's Michael Smith Genome Sciences Centre  
BC Cancer Agency  
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,  
Canada, V5Z 4S6  
Tel: 1-604-707-5900 x5406  
Fax: 1-604-876-3561  
Email: robertk@bcgsc.ca  
Plate: LB02023 row: 0 column: 5  
High quality sequence stop: 725.

FEATURES Location/Qualifiers  
source 1. .725  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Hereford"  
/db\_xref="taxon:9913"  
/clone="IMAGE:8248543"  
/sex="male"  
/tissue\_type="Fetal Medulla"  
/dev\_stage="7 months old fetus"  
/lab\_host="ElectroMAX DH10B T1 Phage-Resistant Cells"  
/clone\_lib="GC\_BGC-20"  
/note="Organ: Fetal Medulla; Vector: pCMV SPORT 6.0;  
Site\_1: SalI (5' end of cDNA); Site\_2: NotI (3' end of  
cDNA)"

#### ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 725;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGTGATGCCTGCCGGGCAC 20  
|||||||  
Db 298 CTGTGATGCCTGCCGGGCAC 279

#### RESULT 3

CO895988/c

LOCUS CO895988 745 bp mRNA linear EST 01-SEP-2004  
DEFINITION BovGen\_24313 normal cattle brain Bos taurus cDNA clone  
RZPDp1056H0842Q 5', mRNA sequence.

ACCESSION CO895988

VERSION CO895988.1 GI:51826305

KEYWORDS EST.

SOURCE Bos taurus (cattle).

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 745)

AUTHORS Hennig,S., Janitz,M., Herwig,R. and Williams,J.

TITLE Generation, annotation, evolutionary analysis and database  
integration of 14969 cattle EST clusters

JOURNAL Unpublished (2004)

COMMENT Contact: Hennig S  
laboraty 123, dept.Lehrach  
Max-Planck-Institut fuer Molekulare Genetik  
Ihnestr.63-73, D-14195 Berlin, Germany  
Tel: +49 30 8413 1612  
Fax: +49 30 8413 1380  
Email: hennig@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONFP cluster was selected for sequencing. cDNA clones and filters are distributed via Deutsches Ressourcenzentrum fuer Genomforschung GmbH (<http://www.rzpd.de>).

PCR Primers

FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq

BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGATGTG 3' (M13FSP) 3'-seq

Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' (M13RSP).

FEATURES

source

Location/Qualifiers

1. .745  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /clone="RZPDp1056H0842Q"  
 /sex="female"  
 /tissue\_type="brain tissue"  
 /dev\_stage="adult brain"  
 /clone\_lib="normal cattle brain"  
 /note="Organ: brain; Vector: pSport1; Site\_1: NotI;  
 Site\_2: SalI; Random primed and directionally cloned in  
 pSport1 vector using NotI  
 (5'-pGACTAGTTCTAGATCGCGAGCGCCGCC (T)15-3' and SalI 5'-  
 TCGACCCACGCTCCG-3' adapters (Gibco BRL))"

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 0.63;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 CTGTGATGCCTGCCGGGCAC 20
Db	269 CTGTGATGCCTGCCGGGCAC 250